WHAT IS CLAIMED IS:

1. An *in vitro* system capable of recapitulating regulated RNA turnover of an exogenously added preselected target RNA sequence comprising a cell extract and said target RNA sequence.

2. The system of claim 1 wherein said regulated RNA ~~turnover~~ deadenylation and degradation is selected from the group consisting of AU-rich element regulated RNA ~~turnover~~ deadenylation and degradation and C-rich element regulated RNA ~~turnover~~ deadenylation and degradation.

3. The system of claim 1 wherein said cell extract is isolated from lysed eukaryotic cells or tissues.

4. The system of claim 3 wherein said cell extract is obtained from a cell line selected from the group consisting of HeLa cells and a T cell line.

5. The system of claim 1 wherein said cell extract is prepared from cells comprising foreign nucleic acid.

6. The system of claim 1 wherein said cell extract is prepared from cells which are uninfected, stably transfected, or transiently transfected.

7. The system of claim 1 wherein said cell extract is partially purified.

8. The system of claim 1 wherein said cell extract is depleted of activity of proteins that bind polyadenylate.

9. The system of claim 8 wherein said cell extract depleted of activity of proteins that bind polyadenylate is prepared by a method selected from the group consisting of:

(a) addition to said system of polyadenylate competitor RNA;

(b) sequestration of proteins that bind polyadenylate;

(c) addition of a proteinase that inactivates a protein that ~~bind~~ binds to polyadenylate; and

(d) addition of an agent that prevents the interaction between polyadenylate and an endogenous macromolecule that binds to polyadenylate.

10. The system of claim 9 wherein said sequestration of proteins that bind polyadenylate is achieved by treatment of said extract with ~~an~~ material that depletes macromolecules that bind polyadenylate selected from the group consisting of antibodies to proteins that bind polyadenylate, polyadenylate, and the combination thereof.

11. The system of claim 10 wherein said material is attached to a matrix.

12. The system of claim 1 wherein said target RNA sequence is selected from the group consisting of synthetic RNA, naturally occurring RNA, messenger RNA, chemically modified RNA, and RNA/DNA derivatives.

13. The system of claim 12 wherein said target RNA sequence comprises a 5' cap and a 3' polyadenylate sequence.

14. The system of claim 1 wherein said target RNA sequence is selected from the group consisting of unlabeled target RNA sequence, labeled target RNA sequence, and the combination thereof.

15. The system of claim 14 wherein said labeled target RNA sequence is labeled with a moiety ~~is~~ selected from the group consisting of a fluorescent moiety, a visible moiety, a radioactive moiety, a ligand, and a combination of fluorescent and quenching moieties.

16. The system of claim 1 additionally comprising exogenously added nucleotide triphosphate.

17. The system of claim 16 wherein said nucleotide triphosphate is ATP.

18. The system of claim 1 further comprising a reaction enhancer.

19. The system of claim 18 wherein said reaction enhancer is selected from the group consisting of polyvinyl alcohol, polyvinylpyrrolidone and dextran.

20. The system of claim 19 wherein said reaction enhancer is polyvinyl alcohol.

21. A method for identifying an agent capable of modulating the stability of a target RNA sequence comprising

(A) providing the system of claim 1;

(B) introducing said agent into said system;

(C) determining the extent of ~~turnover~~ of said target RNA sequence; and

(D) identifying an agent able to modulate the extent of said turnover as capable of modulating the stability of said target RNA sequence.

22. The method of claim 21 wherein said system additionally comprises nucleotide triphosphate.

23. The method of claim 22 wherein said nucleotide triphosphate is ATP.

24. The method of claim 21 wherein said agent is an RNA stability modifying molecule.

25. The method of claim 21 wherein said target RNA sequence is selected from the group consisting of unlabeled target RNA sequence, labeled target RNA sequence, and the combination thereof.

26. The method of claim 25 wherein said labeled RNA sequence is labeled with a moiety ~~is~~ selected from the group consisting of a fluorescent moiety, a visible moiety, a radioactive moiety, a ligand, and a combination of fluorescent and quenching moieties.

27. The method of claim 21 wherein said ~~monitoring~~ the extent of ~~turnover~~ of said target RNA sequence comprises determining the extent of degradation of said labeled target RNA.

28. The method of claim 21 wherein said modulating the stability of a target RNA sequence increases the stability of said target RNA sequence.

29. The method of claim 21 wherein said modulating the stability of a target RNA sequence decreases the stability of said RNA sequence.

30. The method of claim 21 wherein said agent is capable of modulating the activity of a AU rich element binding protein or a C-rich element binding protein.

31. The method of claim 30 wherein said AU rich element binding protein is selected from the group consisting of a member of the ELAV protein family; AUF1; tristetrapolin; AUH; TIA; TIAR; glyceraldehyde-3-phosphate; hnRNP C; hnRNP A1; AU-A; and AU-B.

32. The method of claim 31 wherein said member of the ELAV protein family is selected from the group consisting of HuR, Hel-N1, HuC and HuD.

33. A method for identifying an agent capable of modulating the stability of a target RNA sequence in the presence of an exogenously added RNA stability modifier comprising

(a) providing the system of claim 1;

(b) introducing said RNA stability modifier into said system;

(c) introducing said agent into said system;

(d) determining the extent of ~~turnover~~ of said target RNA sequence; and

(e) identifying an agent able to modulate the extent of said ~~turnover~~ as capable of modulating the stability of said target RNA sequence in the presence of said exogenously added RNA stability modifier.

34. The method of claim 33 wherein said system additionally comprises nucleotide triphosphate.

35. The method of claim 34 wherein said nucleotide triphosphate is ATP.

36. The method of claim 33 wherein said target RNA sequence is selected from the group consisting of unlabeled target RNA sequence, labeled target RNA sequence, and the combination thereof.

37. The method of claim 36 wherein said labeled RNA sequence is labeled with a moiety is selected from the group consisting of a fluorescent moiety, a visible moiety, a radioactive moiety, a ligand, and a combination of fluorescent and quenching moieties.

38. The method of claim 33 wherein said determining the extent of turnover of said target RNA sequence comprises determining the extent of degradation of said labeled target RNA.

39. The method of claim 33 wherein said RNA stability modifier increases the stability of said target RNA sequence.

40. The method of claim 39 wherein said agent decreases the stability of said target RNA sequence increased by said RNA stability modifier.

41. The method of claim 33 wherein said RNA stability modifier decreases the stability of said target RNA sequence.

42. The method of claim 41 wherein said agent increases the stability of said target RNA sequence decreased by said RNA stability modifier.

43. The method of claim 33 wherein said agent is capable of modulating the activity of a AU rich element binding protein or a C-rich element binding protein.

44. The method of claim 43 wherein said AU rich element binding protein is selected from the group consisting of a member of the ELAV protein family; AUF1; tristetrapolin; AUH; TIA; TIAR; glyceraldehyde-3-phosphate; hnRNP C; hnRNP A1; AU-A; and AU-B.

45. The method of claim 44 wherein said member of the ELAV protein family is selected from the group consisting of HuR, Hel-N1, HuC and HuD.

46. A method for identifying an agent capable of modulating the deadenylation of a target RNA sequence comprising

(A) providing the system of claim 1 in the absence of a nucleotide triphosphate;

(B) introducing said agent into said system;

(C) monitoring the deadenylation of said target RNA sequence in said system; and

(D) identifying an agent able to modulate the extent of said deadenylation as capable of modulating the deadenylation of said target RNA sequence.

47. A method for identifying an agent capable of modulating ~~the~~ regulated deadenylation and degradation of a target RNA sequence comprising

(A) providing the system of claim 1 in the presence of a nucleotide triphosphate;

(B) introducing said agent into said system;

(C) monitoring the deadenylation and degradation of said target RNA sequence in said system; and

(D) identifying an agent able to modulate the extent of said deadenylation and degradation as capable of modulating the deadenylation and degradation of said target RNA sequence.

48. A method for identifying an agent capable of modulating cell growth or cell differentiation in a mammal comprising determining the ability of said agent to modulate the stability of a target RNA sequence involved in the modulation of cell growth or differentiation in accordance with claim 21.

~~49. The method of claim 48 wherein said agent capable of modulating cell growth or cell differentiation intervenes in cellular transformation.~~

50. The method of claim 48 wherein said agent ~~capable of modulating~~ cell growth or cell differentiation intervenes in immune dysregulation.

51. A method for identifying, characterizing or isolating an endogenous molecule suspected of participating in the deadenylation or degradation of RNA or regulation thereof comprising

(A) providing the system of claim 1;

(B) introducing said ~~protein~~ suspected of participating in the regulation of RNA ~~turnover~~ into said system;

(C) monitoring the stability of said target RNA sequence in said system; and

(D) identifying, characterizing or isolating said endogenous molecule able to modulate said deadenylation or degradation as capable of participating in the deadenylation or degradation of RNA or regulation thereof.

52. The method of claim 51 wherein said molecule suspected of participating in the deadenylation or degradation of RNA or regulation thereof is protein or RNA.

53. A kit for monitoring the stability of a preselected target RNA sequence under conditions capable of recapitulating regulated RNA turnover, said kit comprising:

(a) cell extract depleted of activity of proteins that bind polyadenylate;

(b) other reagents; and

(c) directions for use of said kit.

54. The kit of claim 53 further comprising nucleotide triphosphates, a reaction enhancer, a target RNA sequence, or any combination thereof.

55. A method for identifying an agent capable of modulating the degradation of a target RNA sequence in the absence of deadenylation comprising

(A) providing a cell extract in the presence of a nucleotide triphosphate;

(B) introducing said agent into said cell extract; and

(C) monitoring the degradation of said target RNA sequence in said extract.